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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
08/487,283	06/07/95	EVANS M	ALX-152.1CIP

18M1/1224

SETH A FIDEL
ALEXION PHARMACEUTICALS
25 SCIENCE PARK
SUITE 360
NEW HAVEN CT 06511

EXAMINER	
GAMBEL, P	

ART UNIT	PAPER NUMBER
1806	

DATE MAILED: 12/24/96

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

08/487,283 06/07/95 EVANS M ALX-152.1CIP

08/487283

DEA/FCE-1994

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
08/487,283	06/07/95	EVANS M	ALX-152.1CIP

SETH A FIDEL
ALEXION PHARMACEUTICALS
25 SCIENCE PARK
SUITE 360
NEW HAVEN CT 06511

18M1/1224 GAMBEL, P

1806

EXAMINER	12/24/96
ART UNIT	PAPER NUMBER
	4

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821-1.825. However, this application fails to comply with the requirements set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures.

The communication filed on 10/26/95 is not fully responsive to the communication mailed 8/25/95 for the reasons(s) set forth on the attached Notice to Comply with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequences Disclosures.

See marked up copy of Raw Sequence Listing.

Applicant must provide: (1) An initial or substitute computer readable form (CRF) copy of the Sequence Listing and (2) A statement that the context of the paper and computer readable copies are the same and where applicable include no new matter, as required by 37 CFR 1.821 (b),(d),(e),(f) or (g).

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, applicant is required to complete the response within a time limit of one month from the date of this letter, 37 CFR 1.135(c). Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Applicant is requested to return a copy of the attached Notice To Comply with the response.

Applicant is required to fulfill these requirements.

Any inquiry concerning this communication should be directed to Examiner Phillip Gambel, Art Unit 1806, whose telephone number is (703) 308-3997.

Phillip Gambel
12/19/96

Application No. 08/487283

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).

☑ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7.

Other: _____

Applicant must provide:

☑ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☑ A statement that the content of ~~the paper~~ and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-~~1123~~ 1216
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

see pp. 2, 3, 10

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

(1) General Information:

(i)APPLICANT: Evans, Mark J.
Matis, Louis A.
Mueller, Eileen Elliott
Nye, Steven H.
Rollins, Scott
Rother, Russell P.
Springhorn, Jeremy P.
Squinto, Stephen P.
Thomas, Thomas C.
Wilkins, James A.

(ii)TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:
(A)ADDRESSEE: Seth A. Fidel
(B)STREET: 25 Science Park (Alexion)
(C)CITY: New Haven
(D)STATE: Connecticut
(E)COUNTRY: USA
(F)ZIP: 06511

(v)COMPUTER READABLE FORM:
(A)MEDIUM TYPE: 3.5 inch, 1.4Mb storage
(B)COMPUTER: Macintosh Cetris 610
(C)OPERATING SYSTEM: System 7
(D)SOFTWARE: WordPerfect 3.0
(vi)CURRENT APPLICATION DATA:
(A)APPLICATION NUMBER:08/487,283
(B)FILING DATE: June 7, 1995
(vii)PRIOR APPLICATION DATA:
(A)APPLICATION NUMBER: US 08/236,208
(B)FILING DATE: 02-MAY-1994

(viii)ATTORNEY/AGENT INFORMATION:
(A)NAME: Seth A. Fidel.
(B)REGISTRATION NUMBER: 38,449
(C)REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
(ix)TELECOMMUNICATION INFORMATION:

(A)TELEPHONE: (203)776-1790
(B)TELEFAX: (203)772-3655

ERRORED SEQUENCES FOLLOW:

(2) INFORMATION FOR SEQ ID NO:1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
--> **(A) DESCRIPTION: KSSKC peptide**
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser
5 10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
15 20

---

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
--> **(A) LENGTH: 1658 Amino Acids**
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
--> **(A)DESCRIPTION: Pro-C5 Polytpeptide**
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Haviland, D.L.
Haviland, J.C.
Fleischer, D.T.
Hunt, A.
Wetsel, R.A.

(B) TITLE: Complete cDNA Sequence of Human
Complement Pro-C5
(C) JOURNAL: Journal of Immunology
(D) VOLUME: 146

(F) PAGES: 362-368
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
                Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
                            -15                 -10

Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
            -5                -1                   5

Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
            10                  15                  20

Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
                25                  30

Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr
 35                  40                  45

Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln
      50                  55                  60

Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly
          65                  70                  75

Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser
            80                  85                  90

Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp
                95                 100

Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr
105                 110                 115

Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp
     120                 125                 130

Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile
          135                 140                 145

Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp
            150                 155                 160

His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser
                165                 170

Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys
175                 180                 185

Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys
     190                 195                 200
```

```
145
146  Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu
147          205                 210                 215
148
149  Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
150              220                 225                 230
151
152  Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
153                  235                 240
154
155  Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
156  245                 250                 255
157
158  Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
159      260                 265                 270
160
161  Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
162          275                 280                 285
163
164  Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
165              290                 295                 300
166
167  Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
168                  305                 310
169
170  Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
171  315                 320                 325
172
173  Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
174      330                 335                 340
175
176  Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
177          345                 350                 355
178
179  Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
180              360                 365                 370
181
182  Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
183                  375                 380
184
185  Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
186  385                 390                 395
187
188  Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
189      400                 405                 410
190
191  Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
192          415                 420                 425
193
194  Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
195              430                 435                 440
196
197  Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn
```

```
                    445                 450

His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
455                 460                 465

Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn
    470                 475                 480

Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
        485                 490                 495

Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
            500                 505                 510

Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
                515                 520

Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
525                 530                 535

Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
    540                 545                 550

Leu Gln Val His Leu Ser Pro Asp Ala Asp Ala Tyr Ser Pro
        555                 560                 565

Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
            570                 575                 580

Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
                585                 590

Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
595                 600                 605

Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Gly Leu
    610                 615                 620

Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
        625                 630                 635

Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
            640                 645                 650

Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
                655                 660

Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
665                 670                 675

Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
    680                 685                 690
```

```
Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
        695                 700                 705

Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
            710                 715                 720

Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu
                725                 730

His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg
735                 740                 745

Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val
    750                 755                 760

Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu
        765                 770                 775

Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly
            780                 785                 790

Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp
                795                 800

Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly
805                 810                 815

Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr
    820                 825                 830

Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly
        835                 840                 845

Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr
            850                 855                 860

Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
                865                 870

Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
875                 880                 885

Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
    890                 895                 900

Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
        905                 910                 915

Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
            920                 925                 930

Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg
```

```
304                 935                 940
305
306  Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
307  945                 950                 955
308
309  Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
310      960                 965                 970
311
312  Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
313          975                 980                 985
314
315  Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
316              990                 995                1000
317
318  Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
319                  1005                1010
320
321  Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
322  1015                1020                1025
323
324  Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
325      1030                1035                1040
326
327  Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
328          1045                1050                1055
329
330  Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
331              1060                1065                1070
332
333  Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
334                  1075                1080
335
336  Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
337  1085                1090                1095
338
339  Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
340      1100                1105                1110
341
342  Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
343          1115                1120                1125
344
345  Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
346              1130                1135                1140
347
348  Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
349                  1145                1150
350
351  Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
352  1155                1160                1165
353
354  Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
355      1170                1175                1180
356
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```
357  Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
358           1185                1190                1195
359
360  Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
361                1200                1205                1210
362
363  Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
364                     1215                1220
365
366  Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
367  1225                1230                1235
368
369  Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
370      1240                1245                1250
371
372  Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
373           1255                1260                1265
374
375  Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
376                1270                1275                1280
377
378  Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
379                     1285                1290
380
381  Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
382  1295                1300                1305
383
384  Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
385      1310                1315                1320
386
387  Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
388           1325                1330                1335
389
390  Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
391                1340                1345                1350
392
393  Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
394                     1355                1360
395
396  Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
397  1365                1370                1375
398
399  Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
400      1380                1385                1390
401
402  Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
403           1395                1400                1405
404
405  Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
406                1410                1415                1420
407
408  Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
409                     1425                1430
```

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410
411  Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
412  1435                1440                1445
413
414  Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
415      1450                1455                1460
416
417  Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
418           1465                1470                1475
419
420  Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
421                1480                1485                1490
422
423  Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
424                     1495                1500
425
426  Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
427  1505                1510                1515
428
429  Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
430      1520                1525                1530
431
432  Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
433           1535                1540                1545
434
435  Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
436                1550                1555                1560
437
438  Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
439                     1565                1570
440
441  Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
442  1575                1580                1585
443
444  Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
445      1590                1595                1600
446
447  Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
448           1605                1610                1615
449
450  Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
451                1620                1625                1630
452
453  Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
454                     1635                1640
455
456  Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
457  1645                1650                1655
458
459
460
```

2493 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
--> **(A) LENGTH: 813 base pairs** 783 shown
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: N19/8 scFv (His Tagged)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
ATG GCC AAT ATT GTG CTG ACC CAA TCT CCA 30
Met Ala Asn Ile Val Leu Thr Gln Ser Pro
 1               5                  10

GCT TCT TTG GCT GTG TCT CTA GGG CAG AGG 60
Ala Ser Leu Ala Val Ser Leu Gly Gln Arg
                15                  20

GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 120
Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser
                25                  30

GTT GAT AGT TAT GAC AAT AGT TTT ATG CAC 150
Val Asp Ser Tyr Asp Asn Ser Phe Met His
                35                  40

TGG TAC CAG CAG AAA CCA GGA CAG CCA CCC 180
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
                45                  50

AAA CTC CTC ATC TTT CTT GCA TCC AAC CTA 210
Lys Leu Leu Ile Phe Leu Ala Ser Asn Leu
                55                  60

GAA TCT GGG GTC CCT GCC AGG TTC AGT GGC 240
Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
                65                  70

AGT GGG TCT AGG ACA GAC TTC ACC CTC ACC 270
Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr
                75                  80

ATT GAT CCT GTG GAG GCT GAT GAT GCT GCA 300
Ile Asp Pro Val Glu Ala Asp Asp Ala Ala
                85                  90

ACC TAT TAC TGT CAG CAA AAT AAT GAG GTT 330
Thr Tyr Tyr Cys Gln Gln Asn Asn Glu Val
                95                 100

CCG AAC ACG TTC GGA GGG GGG ACC AAG CTG 360
Pro Asn Thr Phe Gly Gly Gly Thr Lys Leu
```

120 90
150 120
etc.
Zeroes are off

```
2547                    105                 110
2548
2549   GAA ATA AAA CGG ACC GGA GGT GGC GGG TCG 390
2550   Glu Ile Lys Arg Thr Gly Gly Gly Gly Ser
2551                    115                 120
2552
2553   GGT GGC GGG GGA TCG GGT GGC GGA GGG TCG 420
2554   Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
2555                    125                 130
2556
2557   GAC GTC AAG CTC GTG GAG TCT GGG GGA GAC 450
2558   Asp Val Lys Leu Val Glu Ser Gly Gly Asp
2559                    135                 140
2560
2561   TTA GTG AAG CTT GGA GGG TCC CTG AAA CTC 480
2562   Leu Val Lys Leu Gly Gly Ser Leu Lys Leu
2563                    145                 150
2564
2565   TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT 510
2566   Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
2567                    155                 160
2568
2569   AGC TAT TAT ATG TCT TGG GTT CGC CAG ATT 540
2570   Ser Tyr Tyr Met Ser Trp Val Arg Gln Ile
2571                    165                 170
2572
2573   TCA GAG AAG AGG CTG GAG TTG GTC GCA GCC 570
2574   Ser Glu Lys Arg Leu Glu Leu Val Ala Ala
2575                    175                 180
2576
2577   ATT AAT AGT AAT GGT GAT AGC ACC TAC TAT 600
2578   Ile Asn Ser Asn Gly Asp Ser Thr Tyr Tyr
2579                    185                 190
2580
2581   CCA GAC ACT GTG AAG GGC CGA TTC ACC ATC 630
2582   Pro Asp Thr Val Lys Gly Arg Phe Thr Ile
2583                    195                 200
2584
2585   TCC AGA GAC AAT GCC AAG AGC ACC CTG GAT 660
2586   Ser Arg Asp Asn Ala Lys Ser Thr Leu Asp
2587                    205                 210
2588
2589   CTG CAA ATG AGC AGT CTG AAG TCT GAG GAC 690
2590   Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
2591                    215                 220
2592
2593   ACA GCC TTG TAT TTC TGT GTA AGA GAG ACT 720
2594   Thr Ala Leu Tyr Phe Cys Val Arg Glu Thr
2595                    225                 230
2596
2597   TAT TAC TAC GGG ATT AGT CCC GTC TTC GAT 750
2598   Tyr Tyr Tyr Gly Ile Ser Pro Val Phe Asp
2599                    235                 240
```

```
2600
2601   GTC TGG GGC ACA GGG ACC ACG GTC ACC GTC 780
2602   Val Trp Gly Thr Gly Thr Thr Val Thr Val
2603                   245                 250
2604
2605   TCC TCA CTC GAG CAC CAC CAC CAC CAC CAC 810
2606   Ser Ser Leu Glu His His His His His His
2607                   255                 260
2608
2609   TGA                                     813
2610
2611
2612
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/487,283*

DATE: 12/09/96
TIME: 10:03:25

INPUT SET: S10587.raw

Line	Error	Original Text
57	Unknown or Misplaced Identifier	(A) DESCRIPTION: KSSKC peptide
72	Entered (1658) and Calc. Seq. Length (1676) differ	(A) LENGTH: 1658 Amino Acids
76	Unknown or Misplaced Identifier	(A)DESCRIPTION: Pro-C5 Polytpeptide
2495	Entered (813) and Calc. Seq. Length (783) differ	(A) LENGTH: 813 base pairs
2513	# of Sequences for line conflicts w/ running total	GCC ACC ATA TCC TGC AGA GCC AGT GAA AGT 12

08/487,283

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software will be available via computer downloading (details below). Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette*.

The software can be accessed/requested in the following locations:

1) Dial-up access to the Patent and Trademark Office Bulletin Board System.
   Phone number: 703-305-8950
   Cost: Free-of-charge
2) Dial-up access through the Internet. FTP site: ftp.uspto.gov
   Login as "anonymous". Software is in directory /pub/checker
   Cost: Free-of-charge
3) For diskette copies, telephone requests to 703-306-2600.
   Cost: $25.00

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